

ANALYSES DIRECTED TO PDGFD AND USES THEI
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FIGURE 24

Figure 24A

	(1)	10	20	30	40	51	Section 1
Cur2-1.11.1 HC	(1) EVQIVLESGGGILOPGGSIRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI						
VH3-53	(1) EVQIVLESGGGILOPGGSIRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI						
Consensus	(1) EVQIVLESGGGILOPGGSIRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI						Section 2
	(52)	60	70	80	90	102	
Cur2-1.11.1 HC	(52) YSGGSTYYADSVRGRFTISRDNSKNTLYLOMNSIRRAEDTAVYYCAGTVTTN						
VH3-53	(52) YSGGSTYYADSVRGRFTISRDNSKNTLYLOMNSIRRAEDTAVYYCAGTVTTN						
Consensus	(52) YSGGSTYYADSVRGRFTISRDNSKNTLYLOMNSIRRAEDTAVYYCAGTVTTN						Section 3
	(103)	103	110	120			
Cur2-1.11.1 HC	(103) YYYGMDVWGQGTTVTvss	SEQ ID NO:15					
VH3-53	(98) -----	SEQ ID NO:5					
Consensus	(103)						

Figure 24B

	(1)	10	20	30	40	51	Section 1
CUR2-1.11.1 LC	(1) DIVMTQSPLSLPVTPGEPAISCRSSQSLL SNGYNYLDWYLQKPGQ8PQL						
A19	(1) DIVMTQSPLSLPVTPGEPAISCRSSQSLL SNGYNYLDWYLQKPGQ8PQL						
Consensus	(1) DIVMTQSPLSLPVTPGEPAISCRSSQSLL SNGYNYLDWYLQKPGQ8PQL						Section 2
	(52)	60	70	80	90	102	
CUR2-1.11.1 LC	(52) LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEVGVYVYCMQALQTLP						
A19	(52) LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEVGVYVYCMQALQTLP						
Consensus	(52) LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEVGVYVYCMQALQTLP						Section 3
	(103)	103	111				
CUR2-1.11.1 LC	(103) GGGTKVEIK SEQ ID NO:16						
A19	(101) ----- SEQ ID NO:8						
Consensus	(103)						

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FIGURE 25

Figure 25A

						Section 1
	10	20	30	40	50	
CR2-1.17.1 HC	(1) QVOLVESGGVVQPGSLRLSCAABGPTFSSYGMHWVROAPGKGLEWVAI					
VH-3-33	(1) QVOLVESGGGVQPGSLRLSCAABGPTFSSYGMHWVROAPGKGLEWVAI					
Consensus	(1) QVOLVESGGVVQPGKSLRLSCAABGPTFSSYGMHWVROAPGKGLEWVAI					
						Section 2
	50	60	70	80	90	100
CR2-1.17.1 HC	(52) WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRRAEDTAVYYCARGQY					
VH-3-33	(52) WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRRAEDTAVYYCARG--					
Consensus	(52) WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRRAEDTAVYYCARG					
						Section 3
	100	110	120			
CR2-1.17.1 HC	(103) RYAGYYYYDYGMDVWQGQTTVTVSS		SEQ ID NO:17			
VH-3-33	(99) -----		SEQ ID NO:4			
Consensus	(103)					

Figure 25B

	Section 1					
	10	20	30	40	50	
CR2-1.17.1 LC	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKR ^L IYAAS					
A30	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKR ^L IYAAS					
Consensus	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKR ^L IYAAS					
	Section 2					
	60	70	80	90	104	
CR2-1.17.1 LC	(53) SIQSGVPSRFSGSGSGTFTLTISIQLQPEDFATYYCLOHNSYP	53	60	70	80	90
A30	(53) SIQSGVPSRFSGSGSGTFTLTISIQLQPEDFATYYCLOHNSYP	53	60	70	80	90
Consensus	(53) SIQSGVPSRFSGSGSGTFTLTISIQLQPEDFATYYCLOHNSYP	53	60	70	80	90
	Section 3					
CR2-1.17.1 LC	(105) EIK SEQ ID NO:18	105	1067			
A30	(96) --- SEQ ID NO:11	96				
Consensus	(105)	105				

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FIGURE 26

Figure 26A

	(1)	10	20	30	40	52	Section 1
CR2-1.18 HC	(1) QVQLVQSGAEVIRKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN						
VH1-8	(1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN						
Consensus	(1) QVOLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN						Section 2
	(53)	53	60	70	80	90	104
CR2-1.18 HC	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSLRSEDTAVYYCAREGIAVA						
VH1-8	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSLRSEDTAVYYCAR-----						
Consensus	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSLRSEDTAVYYCAR						Section 3
	(105)	105	110	126			
CR2-1.18 HC	(105) GTYYYYYGMGVWGQGTTTVSS				SEQ ID NO:19		
VH1-8	(99) -----				SEQ ID NO:1		
Consensus	(105)						

Figure 26B

	(1)	10	20	30	40	53	Section 1
CR2-1.18 LC	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS						
A30	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS						
Consensus	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS						Section 2
	(54)	54	60	70	80	90	106
CR2-1.18 LC	(54) LQSGVPSRFSGSGSGTEFTLTISSLQPEDPATYFCQLQHNSYP-----						
A30	(54) LQSGVPSRFSGSGSGTEFTLTISSLQPEDPATYFCQLQHNSYP-----						
Consensus	(54) LQSGVPSRFSGSGSGTEFTLTISSLQPEDPATYFCQLQHNSYP						Section 3
	(107)	R					
CR2-1.18 LC	(107) R						SEQ ID NO:20
A30	(96) -						SEQ ID NO:11
Consensus	(107)						

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FIGURE 27

Figure 27A

	(1)	10	20	30	40	52	Section 1
Cur2-1.19.1 hc	(1) QVOLVQSGAEVKKPGASVKSCKASGYTFTSYDINWVRQATGQGLEWMGMN						
VH1-8	(1) QVOLVQSGAEVKKPGASVKSCKASGYTFTSYDINWVRQATGQGLEWMGMN						
Consensus	(1) QVOLVQSGAEVKKPGASVKSCKASGYTFTSYDINWVRQATGQGLEWMGMN						
							Section 2
	(53) 53	60	70	80	90	104	
Cur2-1.19.1 hc	(53) PNSGNTGYAOKPQGPVTMTRNTSISTAYMELSSIRSEDTAVYYCARVMITF						
VH1-8	(53) PNSGNTGYAOKPQGPVTMTRNTSISTAYMELSSIRSEDTAVYYCAR-----						
Consensus	(53) PNSGNTGYAOKPQGRVTMTRNTSISTAYMELSSIRSEDTAVYYCAR						
							Section 3
	(105) 105	110	126				
Cur2-1.19.1 hc	(105) GGVIVHYGMDVWGQGTTVTVSS			SEQ ID NO:21			
VH1-8	(99) -----			SEQ ID NO:1			
Consensus	(105)						

Figure 27B

	(1)	10	20	30	40	52	Section 1
Cur2-1.19.1 lc	(1) DIQMTQSPSLSA8VGDRVTITCRASQGIRNDLGWYQQPKRPLIYAA8						
A30	(1) DIQMTQSPSLSA8VGDRVTITCRASQGIRNDLGWYQQPKRPLIYAA8						
Consensus	(1) DIQMTQSPSLSA8VGDRVTITCRASQGIRNDLGWYQQPKRPLIYAA8						
							Section 2
	(53) 53	60	70	80	90	104	
Cur2-1.19.1 lc	(53) SLOSGVPSRFSGSGSGTPTIMTISILOPDPATYYCDQHNSDPCSFQGKTL						
A30	(53) SLOSGVPSRFSGSGSGTPTIMTISILOPDPATYYCDQHNSDPCSFQGKTL						
Consensus	(53) SLOSGVPSRFSGSGSGTDFTLTISSLQPEDPATYYCDQHNSP						
							Section 3
	(105) 1097						
Cur2-1.19.1 lc	(105) EIR			SEQ ID NO:22			
A30	(96) ---			SEQ ID NO:11			
Consensus	(105)						

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FIGURE 28

Figure 28A

	1	10	20	30	40	51	Section 1
Cur2-1.23.1_HC	(1)						
VH5-51	(1)	EVOLVQSGAEVKKPGEALKIISCKGSGVFTLWVQVQDQGKGLWMGII					
Consensus	(1)	EVOLVQSGAEVKKPGEALKIISCKGSGVFTLWVQVQDQGKGLWMGII					
	(52)	60	70	80	90	102	Section 2
Cur2-1.23.1_HC	(52)	YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSLKASDTAMYCCARHVSY					
VH5-51	(52)	YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSLKASDTAMYCCARHVSY					
Consensus	(52)	YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSLKASDTAMYCCARHVSY					Section 3
	(103)	103	110	126			
Cur2-1.23.1_HC	(103)	YYVSGSYYNVFDYWGQGTLTVVSS					SEQ ID NO:23
VH5-51	(99)	-----					SEQ ID NO:6
Consensus	(103)	YYVSGSYYNVFDYWGQGTLTVVSS					

Figure 28B

	1	10	20	30	40	51	Section 1
Cur2-1.23.1_LC	(1)						
A30	(1)	DIQMTQSPSLSASVGDRVTITCRASQSRNDLGWYQQIPGKAPKRLIYAA					
Consensus	(1)	DIQMTQSPSLSASVGDRVTITCRASQSRNDLGWYQQIPGKAPKRLIYAA					
	(52)	60	70	80	90	102	Section 2
Cur2-1.23.1_LC	(52)	SSILQRGIVPSEHSGSGCTEFTLTISIQLPEDFATYYCLOHNNSYFTGGGT					
A30	(52)	SSILQSGIVPSEHSGSGCTEFTLTISIQLPEDFATYYCLOHNNSYFTGGGT					
Consensus	(52)	SSILQ GPVSRFSGSGSGTEFTLTISIQLPEDFATYYCLOHNNSYFTGGGT					Section 3
	(103)	103 107					
Cur2-1.23.1_LC	(103)	KVEIK					SEQ ID NO:24
A30	(96)	-----					SEQ ID NO:11
Consensus	(103)	KVEIK					

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FIGURE 29

Figure 29A

										Section 1
	(1)	1	10	20	30	40	50			
CR2-1.24.1_HC	(1)	QVQLVE	SGGGVVQPGRLSIRLSCAASGF	F	SSY	G	MHWWVRQAPGKGLEWVA	I		
VH3-33	(1)	QVOLVES	GGGVVQPGRLSIRLSCAASGF	F	SSY	G	MHWWVRQAPGKGLEWVA	I		
Consensus	(1)	QVQLVE	SGGGVVQPGRLSIRLSCAASGF	P	S	S	YGMHWWVRQAPGKGLEWVA	I		
										Section 2
	(52)	52	60	70	80	90				102
CR2-1.24.1_HC	(52)	WYDGSNKYYADSVKGRFTI	S	RDN	S	KNTLYLQMN	S	R	A	E
VH3-33	(52)	WYDGSNKYYADSVKGRFTI	S	RDN	S	KNTLYLQMN	S	R	A	E
Consensus	(52)	WYDGSNKYYADSVKGRFTI	S	RDN	S	KNTLYLQMN	S	R	A	E
										Section 3
	(103)	103	110	126						
CR2-1.24.1_HC	(103)	SYGYVYYDY	GMDVWGQGTTVTVSS							SEQ ID NO:25
VH3-33	(99)	-	-							SEQ ID NO:4
Consensus	(103)	-	-							

Figure 29B

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FIGURE 30

Figure 30A

	(1)	10	20	30	40	51	Section 1
VH5-51	(1) EVOLVQSGAEVKPGESLKRISCKGSYFTSYWIGWVRQMPGKGLBWMGII						
CR2-1.25.1_HC	(1) EVOLVQSGAEVKPGESLKRISCKGSYFTSYWIGWVRQMPGKGLBWMGII						
Consensus	(1) EVOLVQSGAEVKPGESLKRISCKGSYFTSYWIGWVRQMPGKGLBWMGII						
	(52)	60	70	80	90	102	Section 2
VH5-51	(52) YPGDSDTRYSPSFQGVTTISADKSISTAYLQWSSLKASDTAMYCAR---						
CR2-1.25.1_HC	(52) YPGDSDTRYSPSFQGVTTISADKSISTAYLQWSSLKASDTAMYCARHGSY						
Consensus	(52) YPGDSDTRYSPSFQGVTTISADKSISTAYLQWSSLKASDTAMYCAR						
	(103)	103	110	126			Section 3
VH5-51	(99) -----				SEQ ID NO:6		
CR2-1.25.1_HC	(103) YYGSETYYNVFDYWGQGTLTVSS				SEQ ID NO:27		
Consensus	(103)						

Figure 30B

	(1)	10	20	30	40	52	Section 1
A30	(1) DIQMTQSPSLSASVGDRVTITCRABOGIRNDLGWYQQKPGKAPKRRLIYAA						
CR2-1.25.1_LC	(1) DIQMTQSPSLSASVGDRVTITCRASOGIRNDLGWYQQKPGKAPKRRLIYAA						
Consensus	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRRLIYAA						
	(53)	60	70	80	90	104	Section 2
A30	(53) SIQSGVPSRFSRGSGSGTEFTLTISLOPEDFATTYC1QHNSYP-----						
CR2-1.25.1_LC	(53) SIQSGVPSRFSRGSGSGTEFTLTISLOPEDFATTYC1QHNSYPWTFGQGTV						
Consensus	(53) SIQSGVPSRFSRGSGSGTEFTLTISLOPEDFATTYC1QHNSYP						
	(105)	1087					Section 3
A30	(96) ---				SEQ ID NO:11		
CR2-1.25.1_LC	(105) EIK				SEQ ID NO:28		
Consensus	(105)						

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FIGURE 31

Figure 31A

						Section 1
	1	10	20	30	40	52
VH5-51 CR2-1.29_HC Consensus	(1) EVQLVQSGAERVKKPGESLWIKISCKGSGLYBPTSEWEELGIVRQMEKGELDWMGITY					
	(1) EVQLVQSGAERVKKPGESLWIKISCKGSGLYBPTSEWEELGIVRQMEKGELDWMGITY					
	(1) EVQLVQSGAERVKKPGESLWIKISCKGSGLYBPTSEWEELGIVRQMEKGELDWMGITY					
						Section 2
	53	60	70	80	90	104
VH5-51 CR2-1.29_HC Consensus	(53) PGDSLDTRYSPSFQGQVITISADKSISTAYLOWSSIRAKSDTAMYCAR					
	(53) PGDSLDTRYSPSFQGQVITISADKSISTAYLOWSSIRAKSDTAMYCAR					
	(53) PGDSLDTRYSPSFQGQVITISADKSISTAYLOWSSIRAKSDTAMYCAR					
						Section 3
	105	110	129			
VH5-51 CR2-1.29_HC Consensus	(105) TIGGYYYYYYHGMDVWGQGTTVTVSS					SEQ ID NO:6
	(99) -----					SEQ ID NO:29
	(105) TIGGYYYYYYHGMDVWGQGTTVTVSS					

Figure 31B

	1	10	20	30	40	50	Section 1
A19	(1) DIVMTQSPLSLPVTPGEPAISCRSSQSLHSNGNYLDWYLOKPGQSPQLI						
CR2-1.29_LC	(1) DIVMTQSPLSLPVTPGEPAISCRSSQSLHSNGNYLDWYLOKPGQSPQLI						
Consensus	(1) DIVMTQSPLSLPVTPGEPAISCRSSQSLHSNGNYLDWYLOKPGQSPQLI						
	54	60	70	80	90	106	Section 2
A19	(54) XTCGSRRA3GVDPDRFSGSGCTDFTLKRISRVEA	DIVGTYCMQALQS	P-----				
CR2-1.29_LC	(54) YLG8NRAS3GPDRFSGSGCTDFTLKRISRVEA	DIVGTYCMQALQS	LMCSFGQ				
Consensus	(54) YLG8NRAS3GPDRFSGSGCTDFTLKRISRVEADDVGVYYCMQALQS						
	107	107	113				Section 3
A19	(101) -----	SEQ ID NO:8					
CR2-1.29_LC	(107) GTKLEIR	SEQ ID NO:30					
Consensus	(107)						

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FIGURE 33

Figure 33A

	(1)	10	20	30	40	51	Section 1
VH3-33	(1) QVQLVESGGGVVQPGRSRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAII						
CR2-1.38.1_HC	(1) QVQLVESGGGVVQPGRSRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAII						
Consensus	(1) QVQLVESGGGVVQPGRSRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAII						
	(52)	60	70	80	90	102	Section 2
VH3-33	(52) WYDGGSNEYVADSVVGRTE	ERDNEKNTLYLQMNSLRRAEDTAVYYCAR					
CR2-1.38.1_HC	(52) WYDGNDKRYVADSVVGRTE	ERDNEKNTLYLQMNSLRRAEDTAVYYCAR					
Consensus	(52) WYDG RYYADSVKGRPTISRDNSKNTLYLQMNSLRRAEDTAVYYCAR						
	(103)	103	110	127			Section 3
VH3-33	(99) -----				SEQ ID NO:4		
CR2-1.38.1_HC	(103) DSSDYLYYYYGMDVWGQGTTTVSS				SEQ ID NO:33		
Consensus	(103)						

Figure 33B

	(1)	10	20	30	40	52	Section 1
A20	(1) DIOMTCSPSSLSAVGDRVITCRASQGISNYLAWYQQKPGKVPKLLIYAA						
CR2-1.38.1_LC	(1) DIQMTQSPSSLSAVGDRVITCRASQGISNYLAWYQQKPGKVPKVENLLIYAA						
Consensus	(1) DIQMTQSPSSLSAVGDRVITCRASQGISNYLAWYQQKPGKVPKLLIYAA						
	(53)	60	70	80	90	104	Section 2
A20	(53) TLQSGVPSRFSRGSGSGTDFSLTISSLOPEDVAATLYCOKYNSAE-----						
CR2-1.38.1_LC	(53) TLQSGVPSRFSRGSGSGTDFSLTISSLOPEDVAATLYCOKCNSAEWTFGQGTTV						
Consensus	(53) TLQSGVPSRFSRGSGSGTDFSLTISSLOPEDVAATLYCOK NSAE						
	(105)	1087					Section 3
A20	(96) ---				SEQ ID NO:9		
CR2-1.38.1_LC	(105) EIK				SEQ ID NO:34		
Consensus	(105)						

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FIGURE 34

Figure 34A

	1	10	20	30	40	51	Section 1
VH5-51	(1)						
CR2-1.39.1_HC	(1)	EVQLVQSGAEVKKPGE8IK18CKGSGY8PTSYWIGWVRQMPGKGLEWMGI					
Consensus	(1)	EVQLVQSG EVKKPGE8IK18CKGSGY	PTSYWIGWVRQMPGKGLEWMGI				
	52	60	70	80	90	102	Section 2
VH5-51	(52)	YPGDSDDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR					
CR2-1.39.1_HC	(52)	YPGDSDDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR					
Consensus	(52)	YPGDSDDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR					Section 3
	103	110		126			
VH5-51	(103)	(99) -----					SEQ ID NO:6
CR2-1.39.1_HC	(103)	YYNSGSYYNVFDYWQGTLTVSS					SEQ ID NO:35
Consensus	(103)						

Figure 34B

	1	10	20	30	40	52	Section 1
A30	(1)						
CR2-1.39.1_LC	(1)	DIQMTQSPSISASAVGDRVITTCRASQGIRNDLGWYQQKPGKAPKRLLIYAAAS					
Consensus	(1)	DIQMTQSPSISASAVGDRVITTCRASQGIRNDLGWYQQKPGKAPKRLLIYAAAS					
	53	60	70	80	90	104	Section 2
A30	(53)	SLQSGVPSRFSGSGSTEFITLTISLOPEDFATYYCLOHNSYP					
CR2-1.39.1_LC	(53)	SLQSGVPSRFSGSGSTEFITLTISLOPEDFATYYCLOHNSYPWTFQGQTKV					
Consensus	(53)	SLQSGVPSRFSGSGSTEFITLTISLOPEDFATYYCLOHNSYP					Section 3
	105	1087					
A30	(105)	(96) ---					SEQ ID NO:11
CR2-1.39.1_LC	(105)	EIK					SEQ ID NO:36
Consensus	(105)						

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FIGURE 35

Figure 35A

						Section 1
	10	20	30	40	50	
VH1-8	(1) 1					
CR2-1.45_HC	(1) OQELVQGICAPVKRKGAG3WV8CKL	SGYTFTSYDINWVRQATGQGLEWMGWHN				
Consensus	(1) QVISVSGEAVKRPAGAVRVSCKASGYFTSYDINWVRQATGQGLEWMGWNN					
						Section 2
	60	70	80	90	104	
VH1-8	(53) 53					
CR2-1.45_HC	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSRLSEDATAVYYCAR					
Consensus	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSRLSEDATAVYYCARGSGY					
						Section 3
	105	110	125			
VH1-8	(99) --			SEQ ID NO:1		
CR2-1.45_HC	(105) GYDYYGMDVWGQGTTVTVSS			SEQ ID NO:38		
Consensus	(105)					

Figure 35B

		Section 1				
		10	20	30	40	53
CR2-1.45_LC	A20	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIVSNYLAWYQQKPGKVPKLLIYAAST				
	Consensus	(1) DIQMTQSPSSLSASVGDRVTI	CRASQGISN	LAWYQQKPGKVPKLLIYAAST		
						Section 2
		54	60	70	80	106
CR2-1.45_LC	A20	(54) DQSGVNEKTRIGSGSGSGTDFLTITRISQHOPDVAVYYCQKYNSAP				
	Consensus	(54) DQLCIPTDSESGSGSGTDFLTITRISQHOPDVAVYYCQKYNSAP				
						Section 3
		(107) R				
CR2-1.45_LC	A20	(95) -	SEQ ID NO:9			
	Consensus	(107) R	SEQ ID NO:39			

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FIGURE 36

Figure 36A

						Section 1
	(1)	10	20	30	40	51
VH1-8	(1) QVQLVQSGAEVKKPGASVKVSCKA SGYFTSYDINWVRQATGQGLEWMGWM					
CR2-1.46.1_HC	(1) QVQLVQSGAEVKKPGASVKVSCKA SGYFTSYDINWVRQATGQGLEWMGWM					
Consensus	(1) QVQLVQSGAEVKKPGASVKVSCKA SGYFTSYDINWVRQATGQGLEWMGWM					
						Section 2
	(52)	52	60	70	80	102
VH1-8	(52) NPN SGN TGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR					
CR2-1.46.1_HC	(52) NPN NGN TGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR					
Consensus	(52) NPN GNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR					
						Section 3
	(103)	103	110	126		
VH1-8	(99) -----					SEQ ID NO:1
CR2-1.46.1_HC	(103) VVTATDYYYGMDVWGQGTTTVSS					SEQ ID NO:40
Consensus	(103)					

Figure 36B

						Section 1
	(1)	10	20	30	40	52
A30	(1) DIOMTQSPSLSASVGDRVTITCRASQGIRNDLIGWYQQKPGKAPKRLLIPAA					
CR2-1.46.1_LC	(1) DIOMTQSPSLSASVGDRVTITCRASQGIRNDLIGWYQQKPGKAPKRLLIPAA					
Consensus	(1) DIOMTQSPSLSASVGDRVTITCRASQGIRNDLIGWYQQKPGKAPKRLLIPAA					
						Section 2
	(53)	53	60	70	80	104
A30	(53) SLOQSGVPSRFSRGSGSGTETLTISLQPEDFATYYCLQHNSYP					
CR2-1.46.1_LC	(53) SLOQSGVPSRFSRGSGSGTETLTISLQPEDFATYYCLQHSGYPPTFGQGTV					
Consensus	(53) SLOQSGVPSRFSRGSGSGTETLTISLQPEDFATYYCLQHSGYPPTFGQGTV					
						Section 3
	(105)	105				
A30	(96) ---					SEQ ID NO:11
CR2-1.46.1_LC	(105) EIK					SEQ ID NO:41
Consensus	(105)					

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FIGURE 37

Figure 37A

	(1)	10	20	30	40	51	Section 1
CR2-1.48.1_HC	(1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISEWVRQAPGQGLEWMGWI						
VH1-18	(1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISEWVRQAPGQGLEWMGWI						
Consensus	(1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISEWVRQAPGQGLEWMGWI						
	(52)	60	70	80	90	102	Section 2
CR2-1.48.1_HC	(52) SAYNGNTNYAQKLQGRVTMTTDSTSTAYMEELRSIRSDDTAVYYCAR-----						
VH1-18	(52) SAYNGNTNYAQKLQGRVTMTTDSTSTAYMEELRSIRSDDTAVYYCAR-----						
Consensus	(52) SAYNGNTNYAQKLQGRVTMTTDSTSTAYMEELRSIRSDDTAVYYCAR-----						
	(103)	103	110	125			Section 3
CR2-1.48.1_HC	(103) YYDGSGYYYYFDYWGQGTIVTVSS				SEQ ID NO:42		
VH1-18	(99) -----				SEQ ID NO:2		
Consensus	(103)						

Figure 37B

	(1)	10	20	30	40	52	Section 1
CR2-1.48.1_LC	(1) DIQMTQSPSASVAVGDRVTITCRABOGLISWVYKQPGKAPKLLIYAA						
L5	(1) DIQMTQSPSASVAVGDRVTITCRABOGLISWVYKQPGKAPKLLIYAA						
Consensus	(1) DIQMTQSPSASVAVGDRVTITCRABOGLISWVYKQPGKAPKLLIYAA						
	(53)	60	70	80	90	104	Section 2
CR2-1.48.1_LC	(53) ILQSGVPSRFSGSGSGTDFTLTISLQPEDFAAYCCQINSFPRTFGQGTKV						
L5	(53) ILQSGVPSRFSGSGSGTDFTLTISLQPEDFAAYCCQINSFP-----						
Consensus	(53) ILQSGVPSRFSGSGSGTDFTLTISLQPEDFAAYCCQINSFP-----						
	(105)	105					Section 3
CR2-1.48.1_LC	(105) EIK						SEQ ID NO:43
L5	(96) ---						SEQ ID NO:7
Consensus	(105)						

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FIGURE 38

Figure 38A

	1	10	20	30	40	51	Section 1
CR2-1.49.1 HC	(1)	CVQLVQSGAEEKPKEASVKAESGTYFTSYDINWVRQATGGLEWMGWM					
VH1-8	(1)	CVQLVQSGAEEKPKEASVKAESGTYFTSYDINWVRQATGGLEWMGWM					
Consensus	(1)	CVQLVQSGAEVKKEASVKSCKASGYTFTSYDINWVRQATGGLEWMGWM					
							Section 2
	52	60	70	80	90	102	
CR2-1.49.1 HC	(52)	NPNSGDTGYAQKFQGRVTMTNTSISTAYMELSSLRSEDTAVYFCARMRDI					
VH1-8	(52)	NPNSGDTGYAQKFQGRVTMTNTSISTAYMELSSLRSEDTAVYFCAR---					
Consensus	(52)	NPNSGDTGYAQKFQGRVTMTNTSISTAYMELSSLRSEDTAVYFCAR					
							Section 3
	103	110	127				
CR2-1.49.1 HC	(103)	VATYYYYFYGMWDWGGQGTTVTVSS					SEQ ID NO:44
VH1-8	(99)	-----					SEQ ID NO:1
Consensus	(103)						

Figure 38B

	1	10	20	30	40	52	Section 1
CR2-1.49.1 LC	(1)	DIVMTQSPLSLPVTPGEPAISCR8Q8LLH8NGYNLDWYL KPGQSPOLL					
A19	(1)	DIVMTQSPLSLPVTPGEPAISCR8Q8LLH8NGYNLDWYL KPGQSPOLL					
Consensus	(1)	DIVMTQSPLSLPVTPGEPAISCR8Q8LLH8NGYNLDWYL KPGQSPOLL					
	53	60	70	80	90	104	Section 2
CR2-1.49.1 LC	(53)	IYLGSRASGVPDRFSGSGSGTDFTLKISRVEAEDEVGVYYCMQALQTP					
A19	(53)	IYLGSRASGVPDRFSGSGSGTDFTLKISRVEAEDEVGVYYCMQALQTP					
Consensus	(53)	IYLGSRASGVPDRFSGSGSGTDFTLKISRVEAEDEVGVYYCMQALQTP					
	105	111					Section 3
CR2-1.49.1 LC	(105)	GTRLEIK					SEQ ID NO:45
A19	(101)	-----					SEQ ID NO:8
Consensus	(105)						

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FIGURE 39

Figure 39A

	1	10	20	30	40	51	Section 1
CR2-1.51.1 HC	(1)						
VH5-51	(1)	EVQLVQSGAEVKKPGESIKISCKGSGYSPTSYWIGWVROMPGRGLEWMGII					
Consensus	(1)	EVQLVQSGAEVKKPGESIKISCKGSGYSPTSYWIGWVROMPGRGLEWMGII					
							Section 2
	(52)	52	60	70	80	90	102
CR2-1.51.1 HC	(52)	YPGDSDA	KSPSTQGQVTISADKSISTAYLQWSSLKASDTAMYCARHYDY				
VH5-51	(52)	YFGDSUT	KSPSTQGQVTISADKSISTAYLQWSSLKASDTAMYCAR-----				
Consensus	(52)	YPGDSD	KYSPSPQGQVTISADKSISTAYLQWSSLKASDTAMYCAR				Section 3
	(103)	103	110	126			
CR2-1.51.1 HC	(103)	VWRNYRYTGWFDPWGQGTLTVSS			SEQ ID NO:46		
VH5-51	(99)	-----			SEQ ID NO:6		
Consensus	(103)						

Figure 39B

	1	10	20	30	40	52	Section 1
CR2-1.51.1 LC	(1)						
A27	(1)	EIVLTQSPGTLSLSPGERATLSCRABOSVSSSYLAWYQQKPGQAPRLLIYGA					
Consensus	(1)	EIVLTQSPGTLSLSPGERATLSCRABOSVSSSYLAWYQQKPGQAPRLLIYGA					
							Section 2
	(53)	53	60	70	80	90	104
CR2-1.51.1 LC	(53)	SNRATGHEDRFSGSGSGTITLTISRLPEPEDFAVYYCQQYGSSTFTPGPTK					
A27	(53)	S RATGIPDRFSGSGSGTITLTISRLPEPEDFAVYYCQQYGSSTFTPGPTK					
Consensus	(53)	S RATGIPDRFSGSGSGTITLTISRLPEPEDFAVYYCQQYGSSTFTPGPTK					Section 3
	(105)	105	08				
CR2-1.51.1 LC	(105)	VDIK			SEQ ID NO:47		
A27	(97)	---			SEQ ID NO:10		
Consensus	(105)						

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FIGURE 40

Figure 40A

						Section 1	
	(1)	10	20	30	40	52	
Cur2-6.4.1 hc	(1) QVQLVQSGAEVRKPGASVKVSKCKASGYTFTSYDINWVRQATGGGLEWMGWIN						
VH1-8	(1) QVQLVQSGAEVKKPGASVKVSKCKASGYTFTSYDINWVRQATGGGLEWMGWIN						
Consensus	(1) QVQLVQSGAEVKKPGASVKVSKCKASGYTFTSYDINWVRQATGGGLEWMGWIN						
						Section 2	
	(53)	53	60	70	80	90	104
Cur2-6.4.1 hc	(53) PNSGNTDYAQKFQGRVTMTRDTTSISTAYMELSSRLSED						
VH1-8	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSRLSED						
Consensus	(53) PNSGNT YAQKFQGRVTMTR TSISTAYMELSSRLSED						
						Section 3	
	(105)	105	110	125			
Cur2-6.4.1 hc	(105) NYDYYYGMDVWGQGTTVTVSS				SEQ ID NO:48		
VH1-8	(99) -----				SEQ ID NO:1		
Consensus	(105)						

Figure 40B

						Section 1	
	(1)	10	20	30	40	52	
Cur2-6.4.1 Lc	(1) EIVLTQSPGTLSLSPGERATLSRASQSVSSSYLAWYQQKPGQAPRLLIYA						
A27	(1) EIVLTQSPGTLSLSPGERATLSRASQSVSSSYLAWYQQKPGQAPRLLIYA						
Consensus	(1) EIVLTQSPGTLSLSPGERATLSRASQSVSSSYLAWYQQKPGQAPRLLIYA						
						Section 2	
	(53)	53	60	70	80	90	104
Cur2-6.4.1 Lc	(53) SSRATGIPDRFSSGSQGTDFTLTISRLPEDFAVYYCQQYGSSECSFGQGTK						
A27	(53) SSRATGIPDRFSSGSQGTDFTLTISRLPEDFAVYYCQQYGSSE						
Consensus	(53) SSRATGIPDRFSSGSQGTDFTLTISRLPEDFAVYYCQQYGSSE						
						Section 3	
	(105)	105	08				
Cur2-6.4.1 Lc	(105) LEIK			SEQ ID NO:49			
A27	(97) -----			SEQ ID NO:10			
Consensus	(105)						